

```

Db      629 CT 630

RESULT 2
AU229698/c
LOCUS   AU229698
DEFINITION AU229698 RAF17 Arabidopsis thaliana cDNA clone RAF17-32-O17 3', mRNA sequence.
ACCESSION AU229698
VERSION   AU229698.1
KEYWORDS  GI:19798174
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 438)
AUTHORS   Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A.,
Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
Mura
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda f1C-l vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified phagescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further
details.

FEATURES
source
1..438
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAF17-32-O17"
/lab_host="DH10B"
/clone_lib="RAF17"
/notes="Site 1: BamHI; Site 2: SalI; Subtraction Library.
The sequence was obtained from samples subjected to
dehydration-treated (1, 2, 5, 10 and 24 hr) and
rehydration-treated (1, 2, 5, 10, and 24 hr after
dehydration treatment)"

ORIGIN
Query Match 19.8%; Score 242; DB 9; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.1e-114; Indels 0; Gaps 0;
Matches 242; Conservative 0; Mismatches 0;

Qy      819 AGGTTCTTTAGGACCATAGGATGTGTTTGGCATCATCACTAGCTTCGTGT 878
Db      819 AGGTTCTTTAGGACCATAGGATGTGTTTGGCATCATCACTAGCTTCGTGT 878
Db      405 AGGTTCTTTAGGACCATAGGATGTGTTTGGCATCATCACTAGCTTCGTGT 346
Qy      879 TCTGATAGTGTCTGTCCTCGGTGACTGAAGTTTCGCGTGTGTTTTCGGGAGAA 938
Db      879 TCTGATAGTGTCTGTCCTCGGTGACTGAAGTTTCGCGTGTGTTTTCGGGAGAA 938
Db      345 TCTGATAGTGTCTGTCCTCGGTGACTGAAGTTTCGCGTGTGTTTTCGGGAGAA 286
Qy      939 GTTTTCAGGCAGAGAAAGGTGTCTCTCTACTTCTTTCTTTCTTTGGGATTTGCTCTTACTT 998
Db      939 GTTTTCAGGCAGAGAAAGGTGTCTCTCTACTTCTTTCTTTCTTTGGGATTTGCTCTTACTT 998
Db      285 GTTTTCAGGCAGAGAAAGGTGTCTCTCTACTTCTTTCTTTCTTTGGGATTTGCTCTTACTT 226
Qy      999 CTACGGCGAGTTTAAATCCGGCAGAAAGTTGTGTGATAAACCTCAACCCGGCAGACAGA 1058
Db      999 CTACGGCGAGTTTAAATCCGGCAGAAAGTTGTGTGATAAACCTCAACCCGGCAGACAGA 1058
Db      225 CTACGGCGAGTTTAAATCCGGCAGAAAGTTGTGTGATAAACCTCAACCCGGCAGACAGA 166

Qy      1059 AC 1060
Db      1059 AC 1060
Db      165 AC 164

RESULT 3
H76984
LOCUS   H76984
DEFINITION H76984 Lambda-PRL2 Arabidopsis thaliana cDNA clone 200N2T7, mRNA sequence.
ACCESSION H76984
VERSION   H76984.1
KEYWORDS  GI:1054235
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 589)
AUTHORS   Newman,T., deRuijn,F.J., Green,P., Keegstra,K., Kende,H.,
Mentchesh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
7846151
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcm@msu.edu
Seg primer: T7 dye primer.
Location/Qualifiers
1..589
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="var Columbia"
/db_xref="taxon:3702"
/clone="200N2T7"
/clone_lib="Lambda-PRL2"
/notes="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA."

ORIGIN
Query Match 14.3%; Score 175; DB 14; Length 589;
Best Local Similarity 99.6%; Pred. No. 2e-79;
Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      55 ATTATCCTCCTATAGGAACATGGAGTCTTTTGTAACTGCTCTCTACTTCCACCAAT 114
Db      55 ATTATCCTCCTATAGGAACATGGAGTCTTTTGTAACTGCTCTCTACTTCCACCAAT 114
Qy      115 GCGGAAACCAATCTGTTTCATGAGTTTCTATCAACCGGTGTTTTCCAATCATCTC 174
Db      115 GCGGAAACCAATCTGTTTCATGAGTTTCTATCAACCGGTGTTTTCCAATCATCTC 174
Qy      175 ATCCCTCTCTGGTCTCTTCTCAGCGTCCGCGCAACCGCAACCTTAAACGCG 234
Db      175 ATCCCTCTCTGGTCTCTTCTCAGCGTCCGCGCAACCGCAACCTTAAACGCG 234
Qy      121 ATCCCTCTCTGGTCTCTTCTCAGCGTCCGCGCAACCGCAACCTTAAACGCG 180
Db      121 ATCCCTCTCTGGTCTCTTCTCAGCGTCCGCGCAACCGCAACCTTAAACGCG 180
Qy      235 GAAACCAACGCGGAAACCAAGCTCTTCTCATGTGAAACTCTCTGT 280

```

Db 181 GAAACAAGCGAACAAGCTTCTCTCATGAACTCCTCTGT 226
|||||

RESULT 4
B2501737/c 807 bp DNA linear GSS 15-DEC-2002
LOCUS BOMFA70TF BO.1.6.2_KB_tot Brassica oleracea genomic clone BOMFA70,
DEFINITION genomic survey sequence.

ACCESSION B2501737
VERSION B2501737.1 GI:27018757
KEYWORDS GSS.

SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 807)
TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOMFA70TF

COMMENTS Contact: Chris Town
TIGR Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

Location/Qualifiers

1..807
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOMFA70"
/clone_lib="BO.1.6.2_KB_tot"
/note="Vector: pHOSt1; Site:1. BstXI; 1.6-2 kb sheared
total DNA inserted into pHOSt1 using BstXI linkers"

ORIGIN
Query Match 3.1%; Score 38; DB 28; Length 807;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 928 TTCGGGAGAGTTTCAGGAGAAAGGTGTCTCTCT 965
|||||

Db 797 TTCGGGAGAGTTTCAGGAGAAAGGTGTCTCTCT 760
|||||

RESULT 5
CC457536 395 bp DNA linear GSS 30-MAY-2003
LOCUS SALK_110605.26.10.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_110605.26.10.x, genomic
survey sequence.

ACCESSION CC457536
VERSION CC457536.1 GI:31219753
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 395)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atg28230.
Class: TDNA tagged.

FEATURES

source

1..395

Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_110605.26.10.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 3.0%; Score 37; DB 28; Length 395;

Best Local Similarity 100.0%; Pred. No. 1.6e-07;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1007 AGTTTAATCCGGCAAGAGTTGTGATAAACCTCA 1043
|||||Db 116 AGTTTAATCCGGCAAGAGTTGTGATAAACCTCA 152
|||||

RESULT 6

BH601144

LOCUS BH601144

DEFINITION BOHJF33TF BOHJ Brassica oleracea genomic clone BOHJF33, genomic

survey sequence.

ACCESSION BH601144

VERSION BH601144.1 GI:17853590

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 784)

TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other GSSs: BOHJF33TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

1..784

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="T01000DH3"

/db_xref="taxon:3712"

/clone="BOHJF33"

/clone_lib="BOHJ"

/note="Vector: pHOSt1; Site:1. BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

ORIGIN